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Characteristics of CDC Group 3 and Group 5 Coryneform Bacteria Isolated from Clinical Specimens and Assignment to the Genus *Dermabacter*

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Over a 1-year period, 11 isolates (including 5 from blood cultures) of the recently described CDC group 3 and group 5 coryneform bacteria were derived from clinical specimens and compared with reference strains. Biochemical characteristics indicated a very close relationship between CDC group 3 and group 5 coryneform bacteria. The ability of CDC group 3 and the inability of CDC group 5 coryneform bacteria to ferment xylose were the only reactions that were different for the two taxa. Chemotaxonomic features of the two groups included the presence of *meso*-diaminopimelic acid, a lack of mycolic acids, and the presence of predominantly branched cellular fatty acids, a combination found among gram-positive rods only in *Brevibacterium* spp., *Brachybacterium faecium*, and *Dermabacter hominis*. 16S rRNA gene sequence analysis revealed that CDC group 3 and group 5 coryneform bacteria are members of the genus *Dermabacter*, which to date has been isolated exclusively from human skin.

In recent years, gram-positive coryneform rods (GPCR) have attracted the attention of clinical microbiologists, mainly because of an increased recognition in clinical material but also because of taxonomic interests (9, 22). The number of defined species and taxa has increased accordingly. In 1992, the Special Bacteriology Reference Laboratory at the Centers for Disease Control and Prevention (CDC), Atlanta, Ga., proposed the new coryneform groups 3 to 7 (16). Up to now, 18 strains of CDC group 3 and 12 strains of CDC group 5 coryneform bacteria, isolated mainly from blood, have been described (16). We report here the recovery of 11 additional strains of CDC group 3 and group 5 coryneform bacteria from clinical specimens over a 1-year period and present their clinical, phenotypic, and genotypic characteristics. On the basis of comparative 16S rRNA gene sequence analysis, we demonstrate CDC group 3 and group 5 coryneform bacteria to be members of the recently described genus *Dermabacter*, containing *Dermabacter hominis* as the only species. To our knowledge, this report for the first time presents data on the clinical relevance of strains belonging to the genus *Dermabacter*.

MATERIALS AND METHODS

Strains, media, and growth conditions. Clinical samples were cultured aerobically at 37°C with 5% CO_2 on Columbia agar with 5% sheep blood (SBA), the same medium containing colistin and nalidixic acid, Columbia chocolate agar, and MacConkey agar without CO_2 (all media were purchased from Becton Dickinson Microbiology Systems, Cockeysville, Md., unless specified otherwise). For anaerobic cultures, brucella agar with 5% sheep blood, kanamycin-vancomycin agar with laked blood, and phenylethyl alcohol blood agar plates were used. Aerobically growing gram-negative rods and gram-positive cocci were identified by established procedures (11, 21). Obligate anaerobes were reported as mixed anaerobic flora if microscopic examination of anaerobic plates revealed more than three morphologically different strains.

CDC group 3 coryneform strains 1 and 2 as well as CDC group 5 coryneform strains 5 and 6 were received from R. E. Weaver, Special Bacteriology Reference Laboratory, CDC, as reference strains. Strains 3 and 4 as well as strains 7 to 15 were isolated in the clinical microbiology laboratories of the Department of Medical Microbiology at the University of Zürich between November 1992 and October 1993. For comparative biochemical testing, we used the type strain of *D. hominis* (NCFB 2769).

Biochemical profiles. Media used for biochemical characterization were prepared as outlined by Nash and Krenz (25). Cystine Trypticase agar medium contained 1% carbohydrates and was supplemented with 5% rabbit serum. Lysine decarboxylase activity was determined with lysine decarboxylase broth and ornithine decarboxylase activity was determined with motility-indole-ornithine medium (both from Difco, Detroit, Mich.). DNase production was tested with DNase test agar with methyl green (Difco). The presence of gelatinase was detected by immersing film strips (Diagnostics Pasteur, Marnes-la-Coquette, France) in bacterial suspensions and incubating them for up to 1 week. Starch hydrolysis was tested on Mueller-Hinton agar after incubation for 2 days at 35°C by flooding the plate with a 1:5 dilution of Lugol iodine solution (14). The commercial galleries API 20E, API CORYNE, and API ZYM (all from API bioMérieux SA, Marcy l'Etoile, France) were used according to the instructions provided by the manufacturer. The CAMP reaction was performed on SBA with *Staphylococcus aureus* ATCC 25923. Incubation was carried out at 37°C without CO_2 for tests dependent on changes in pH; otherwise, incubation was at 37°C in an atmosphere with 5% CO_2.

Susceptibility testing. Six antibiotics (ciprofloxacin, clindamycin, erythromycin, penicillin G, rifampin, and vancomycin)

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TABLE 1. Origins of CDC group 3 and group 5 coryneform bacteria isolated from clinical samples

Strain	Patient's sex and age[a]	Diagnosis or source	Result of direct Gram stain[b]	Result in primary cultures[c]	
				Coryneforms	Others
Group 3					
1	NK	Abscess, mandible	NK	—	—
2	NK	Eye	NK	—	—
3	M, 64	Blood culture, sepsis	ND	1	0
4	F, 53	Blood culture, fever of unknown origin	ND	1	0
Group 5					
5	NK	Blood culture	NK	—	—
6	NK	Blood culture	NK	—	—
7	M, 67	Infected vascular graft	ND	1	1[d]
8	M, 29	Lymphocele after renal transplantation	ND	3	3[d]
9	F, 59	Conjunctivitis	ND	3	3[d]
10	M, 68	Blood culture, fever of unknown origin	ND	1	0
11	F, 31	Blood culture, fever of unknown origin	ND	1	1[d]
12	M, 45	Orchitis, human immunodeficiency virus infection	3 WBC, 0 MO	2	0
13	M, 61	Infected deep wound, lower leg	3 WBC, 3 GNR	3	4[e]
14	M, 61	Infected deep wound, lower leg	3 WBC, 3 GNR	3	5[f]
15	M, 81	Blood culture, fever of unknown origin	ND	1	0

[a] NK, not known; F, female; M, male.
[b] NK, not known; ND, not done; 3, <10 leukocytes (WBC) or microorganisms (MO) per oil immersion field (magnification ×1,000); GNR, gram-negative rods.
[c] —, reference strain; 1, detected in blood culture; 2, detected after enrichment in fluid thioglycolate only; 3, approximately 10^3 CFU/ml were detected; 4, approximately 10^4 CFU/ml were detected; 5, $\geq 10^5$ CFU/ml were detected.
[d] Coagulase-negative staphylococci were detected.
[e] *E. coli* was detected.
[f] Mixed anaerobic flora was detected.

used in the treatment of gram-positive infections as well as four aminoglycosides (amikacin, gentamicin, netilmicin, and tobramycin) were selected for susceptibility testing by the National Committee for Clinical Laboratory Standards agar dilution technique on Mueller-Hinton agar with 5% sheep blood (26).

Gas-liquid chromatography. Volatile and nonvolatile fatty acids from fermentation of glucose by organisms grown in brain heart infusion broth supplemented with 1% glucose were determined by gas-liquid chromatography (15) on a Sigma 300 chromatograph (Perkin-Elmer, Norwalk, Conn.). For analysis of cellular fatty acid (CFA) patterns, we used the Microbial Identification System (Microbial ID, Inc., Newark, Del.) (MIDI). Cultures were grown for 48 h at 37°C with 5% CO_2 on Trypticase soy agar without any additives (TSA) or supplemented with 5% sheep blood (TSBA) (31).

Analysis of cell wall constituents. *meso*-Diaminopimelic acid and mycolic acids in whole-cell hydrolysates were detected by the methods described by Schaal (28).

DNA analysis. Chromosomal DNA was isolated and purified by hydroxyapatite chromatography (6), and the moles percent G+C content was determined by thermal denaturation (24).

For rRNA sequence determination, total genomic DNA was isolated by a standard miniprep method (2). A large fragment of the 16S rRNA gene was amplified by PCR using universal primers pA (nucleotides 8 to 28, *Escherichia coli* numbering [5]) and pH* (nucleotides 1542 to 1522) (4). Direct sequencing of the amplified product was performed by using primers for conserved regions of the rRNA and a Sequenase version 2.0 sequencing kit (United States Biochemical Corp., Cleveland, Ohio) as described previously (18).

Nucleotide sequence accession number. The nucleotide sequence of the 16S rRNA gene of strain 8 has been deposited with GenBank (EMBL) under accession number X76773.

RESULTS

Clinical data are given in Table 1. Seven of the 15 strains were isolated from blood cultures. None of our five blood-derived isolates came from a line-drawn specimen. In only 3 of 11 samples, direct Gram strains had been performed but did not show GPCR. In addition to the GPCR, in 4 of 11 cases coagulase-negative staphylococci and in 1 case each *E. coli* or mixed anaerobic flora were isolated. Strains 13 and 14 were recovered from the same patient at a 2-week interval. Immunosuppression was noted only in 2 of the 10 patients. Eight of 11 strains were from patients hospitalized in seven different medical and surgical wards at the Zürich University Hospital, and three strains came from three other hospitals.

All 15 strains were able to grow under strictly anaerobic conditions. After 24-h incubation at 37°C on SBA, colony sizes ranged from 0.5 to 1.5 mm. Colonies were whitish grey with entire edges. Gram stains revealed relatively small, "coccoid" rods, with no forming of endospores. As evident from Table 2, biochemical features of CDC group 3 and group 5 coryneform bacteria were very similar (for the remainder of this article, the two groups of bacteria are referred to as group 3 and group 5). The only major phenotypic difference between group 3 and group 5 strains was the inability of group 5 strains to ferment xylose. The type strain of *D. hominis* was found to have the same biochemical profile as group 5 strains. Minor differences of group 3 and group 5 isolates were noted for lysine decarboxylase, α-galactosidase, and β-galactosidase. However, even the activities of the other enzymes, as measured with the API ZYM system, were very similar for group 3 and group 5 strains.

The API CORYNE system identified all 15 isolates as CDC group A coryneform bacteria, with good to very good scores (Table 3).

Antimicrobial susceptibility testing revealed similar patterns for group 3 and group 5 strains (Table 4). Vancomycin was found to be the only antimicrobial agent tested to which all 15 strains were susceptible. Group 3 and group 5 strains were variably susceptible to aminoglycosides: strain 1 was resistant to all aminoglycosides tested, and five strains of group 5 were

TABLE 2. Biochemical characteristics of CDC group 3 and group 5 coryneform bacteria

Reaction	% Positive reactions	
	Group 3 (n = 4)	Group 5 (n = 11)
Catalase	100	100
Oxidase	0	0
Motility	0	0
Nitrate reduction	0	0
Urea hydrolysis	0	0
Esculin hydrolysis	100	100
Gelatin hydrolysis	100	100
Starch hydrolysis	100	100
Triple sugar iron slant acid	100	100
Triple sugar iron butt acid	100	100
Fermentation (after 24 h) of:		
Glucose	100	100
Maltose	100	100
Sucrose	100	100
Lactose	100	91
Mannitol	0	0
Xylose	100	0
CAMP test	0	0
DNase	100	100
Citrate utilization	0	0
Lysine decarboxylase	100	82
Ornithine decarboxylase	100	100
Arginine dihydrolase	0	0
Tryptophane desaminase	0	0
Indole production	0	0
Assayed for the following enzyme[a]:		
Alkaline phosphatase	100 (w)	100 (w)
Esterase (C_4)	100 (m)	100 (m)
Esterase lipase (C_8)	100 (s)	100 (s)
Lipase (C_{14})	0	0
Leucine arylamidase	100 (m)	91 (m)
Valine arylamidase	0	0
Cystine arylamidase	75 (w)	64 (w)
Trypsin	0	0
Chymotrypsin	0	0
Acid phosphatase	0	0
Phosphoamidase	0	27 (w)
α-Galactosidase	75 (w)	27 (w)
β-Galactosidase	100 (m)	100 (m)
β-Glucuronidase	0	0
α-Glucosidase	100 (s)	100 (s)
β-Glucosidase	75 (m)	73 (m)
n-Acetyl-β-glucosaminidase	100 (s)	100 (s)
α-Mannosidase	100 (s)	100 (s)
α-Fucosidase	0	0

[a] As determined by the API ZYM system. The amounts of hydrolyzed substrates were designated as follows: w, approximately 5 nmol; m, approximately 20 nmol; s, >40 nmol.

resistant to gentamicin, netilmicin, and tobramycin but remained susceptible to amikacin. These five strains were also found to be resistant to clindamycin and rifampin.

Acetic acid and lactic acid were detected as major end products of glucose metabolism.

Group 3 and group 5 strains could not be separated by their CFA patterns. 12-Methyl-tetradecanoic acid ($C_{ai15:0}$) and 14-methyl-hexadecanoic acid ($C_{ai17:0}$) were shown to be the major CFAs. In both group 3 and group 5, we also detected relatively large amounts of $C_{19:0cyclo\ omega8c}$ CFA (1 to 7%) with the MIDI system when cells were grown on TSBA. However, this fatty acid could not be detected when strains were grown on TSA (Table 5).

TABLE 3. API CORYNE patterns

API CORYNE code and identification rating (no. of strains)	Group or species	No. of mismatched reactions	% ID[a]
Group 3			
4570765; very good (4)	Coryneform group A	2	99.6
	Oerskovia spp.	4	0.4
Group 5			
4570365; good (10)	Coryneform group A	3	98.3
	Oerskovia spp.	4	1.7
4570165; very good (1)	Coryneform group A	3	99.9
	Oerskovia spp.	5	0.1

[a] % ID, percentage of identification, an estimate of how closely the profile corresponds to the taxon relative to all other taxa in the data base.

Cell walls of group 3 and group 5 contained *meso*-diaminopimelic acid, but mycolic acids were not present.

The G+C contents of both group 3 (n = 2) and group 5 (n = 2) strains were found to be 60 to 62 mol%.

Figure 1 depicts the primary 16S rRNA structure of strain 8. Partial sequencing of approximately 600 bases of the 16S rRNA (including variable regions V1 to V3) of strain 3 revealed an almost identical sequence (data not shown).

DISCUSSION

Over a 1-year period, we isolated in our clinical laboratory 11 strains of group 3 and group 5 bacteria. These GPCR were further characterized by biochemical, chemotaxonomic, and molecular methods. A source for these isolates could not be found, but nosocomial transmission seemed most unlikely. However, group 3 and group 5 strains were, in 4 of 11 cases, associated with coagulase-negative staphylococci, suggesting human skin or mucous membranes as a reservoir. For only one patient, a concurrent culture of group 5 bacteria was obtained.

The key reaction to differentiate group 3 and group 5 strains was the fermentation of xylose. None of the other biochemical tests applied proved to be discriminative.

TABLE 4. Antimicrobial susceptibility patterns of CDC group 3 and group 5 coryneform bacteria

Antimicrobial agent	% Susceptible strains[a]		MIC range (μg/ml)
	Group 3 (n = 4)	Group 5 (n = 11)	
Amikacin	75	100	4–>64
Ciprofloxacin	50	27[b]	0.5–4
Clindamycin	75	55	0.03–>64
Erythromycin	75	45[c]	<0.03–4
Gentamicin	75	55	1–>64
Netilmicin	25[d]	45	4–>64
Penicillin G[e]	100	27	<0.03–2
Rifampin	100	55	<0.03–16
Tobramycin	25	9[f]	8–>64
Vancomycin	100	100	0.13–0.5

[a] According to National Committee for Clinical Laboratory Standards interpretive standards (27).
[b] Seven of 11 strains were moderately susceptible.
[c] Six of 11 strains were intermediately susceptible.
[d] One of four strains was intermediately susceptible.
[e] The categories for staphylococci were applied.
[f] One of 11 strains was intermediately susceptible.

TABLE 5. CFA profiles of CDC group 3 and group 5 coryneform bacteria[a]

Component (FAME[b])	% of CFAs (range)[c]	
	Group 3 (n = 4)	Group 5 (n = 11)
$C_{14:0}$	2 ± 1 (1–2)	1 ± 1 (1–2)
$C_{i15:0}$	9 ± 1 (8–11)	9 ± 1 (8–10)
$C_{ai15:0}$	26 ± 7 (17–35)	23 ± 1 (22–24)
$C_{i16:0}$	13 ± 4 (8–16)	15 ± 2 (10–17)
$C_{16:0}$	5 ± 1 (4–7)	5 ± 2 (3–7)
$C_{ai17:0}$	34 ± 7 (30–44)	36 ± 3 (30–39)
$C_{20:1\ omega9t}$	6 ± 1 (4–7)	5 ± 1 (4–7)

[a] Cells were grown on TSA.
[b] FAME, fatty acid methyl ester.
[c] Values are means ± standard deviations. FAMEs with less than 1% were not reported.

In order to place GPCR in their correct taxonomic position, a combination of chemotaxonomic investigations is necessary (12). The combination of *meso*-diaminopimelic acid and mainly branched CFAs in GPCR is found only in *Brevibacterium* spp., *Brachybacterium faecium*, and *D. hominis* (7, 8, 19, 20) (Table 6). However, assignment of group 3 and group 5 strains to the nonfermentative genus *Brevibacterium* (20) can be excluded since group 3 and group 5 are fermentative. *B. faecium* has a significantly higher G+C content (68 to 72 mol%) (7) than group 3 and group 5 strains. Furthermore, *B. faecium* has so far never been isolated from humans but only from poultry deep litter. The biochemical and chemotaxonomic features of group 3 and group 5 strains, however, are in accordance with the original description of *D. hominis* (19). While Jones and Collins (19) described the activities of α-galactosidase and β-glucosidase as negative in *D. hominis*, we detected weak or medium activity, respectively. This discrepancy might be due to the use of different inocula or due to difficulties in reading the API ZYM system, as reported elsewhere (13). Jones and Collins (19) described ornithine decarboxylase as absent in *D. hominis*, whereas we observed strong activity of this enzyme in all 15 strains tested by two independent test systems. Additionally, we found lysine decarboxylase in nearly all group 3 and group 5 strains, an enzyme usually not seen in GPCR (11a). The CDC Special Bacteriology Reference Laboratory described the presence of lysine and ornithine decarboxylases initially only in group 5 strains (16) but subsequently also found group 3 strains positive for both lysine and ornithine (16a). Furthermore, Jones and Collins (19) reported a qualitatively similar but quantitatively different CFA pattern for *D. hominis* (i.e., larger amounts of $C_{ai17:0}$) than we detected in group 3 and group 5 strains. This discrepancy could possibly be attributed to different growth conditions and media (23). Another uncommon feature of group 3 and group 5 strains appeared to be the presence of acid tentatively identified as $C_{19:0cyclo\ omega8c}$ CFA when cells were grown on TSBA. We are not aware of any other GPCR containing such large amounts of this CFA except lactobacilli (3, 30, 31). However, this CFA could not be detected when group 3 and group 5 strains were grown on TSA, suggesting that the CFA data for TSBA did not accurately reflect the biosynthetic potential of these strains.

Due to their absence from the API CORYNE data base (1), group 3 and group 5 strains cannot be identified at present with this system. However, group 3 and group 5 strains can easily be distinguished from CDC group A coryneform bacteria (Table 3), which are motile and produce a yellow pigment (17). Moreover, cell walls of CDC group A coryneform bacteria do not contain *meso*-diaminopimelic acid (11a).

Aminoglycoside resistance is usually not encountered in GPCR except in *Corynebacterium jeikeium* and *Corynebacterium urealyticum* (10), whereas it is widespread in gram-negative rods (29). However, our patients' history did not reveal any prior topical or systemical chemotherapy with aminoglycosides, nor did we observe any increase in aminoglycoside resistance in bacteria originating from hospitals where the specimens came from. At present, it remains unclear whether aminoglycoside resistance was acquired or is intrinsic to the strains examined.

To establish the relatedness of group 3 and group 5 strains with the genus *Dermabacter*, we sequenced the entire 16S rRNA gene of strain 8 and the most characteristic part of the 16S rRNA gene of strain 3. On the basis of a comparison of

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31
CGAACGCTGG CGGCGTGCTT AACACATGCA AGTCGAACGA TGAANCTGTG CTTGCACAGT GGATTAGTGG CGAACGGGTG AGTAACACGT GAGTAACCTG

CCCTCCACTT TGGGATAACT CCGAGAAATC GGGGCTAATA CTGGATATGA CTATGGCCCG CATGGGTTGT GGTGGAAAGT TTTTCGGTGG GGGATGGGCT

CGCGGCCTAT CAGTTTGTTG GTGAGGTAGT GGCTCACCAA GGCGATGACG GGTAGCCGGC CTGAGAGGGC GACCGGCCAC ACTGGGACTG AGACACGGCC

CAGACTCCTA CGGGAGNCAG CAGTGGGGAA TATTGCACAA TGGGCGAAAG CCTGATGCAG CGACGCCGCG TGGGGGATGA CGGCCTTCGG GTTGTAAACC

TCTTTCAGCA AGGAAGAAGC GAAAGTGACG GTACTTGCAG AAGAAGCGCC GGCTAACTAC GTGCCAGCAG CCGCGGTAAT ACGTAGGGCG CAAGCGTTGT

CCAGAATTAT TGGGCGTAAA GGGCTTGTAG GTGGCTTGTC GCGTCTNCCG TGAAAACCCA GGGCTTAACT CTGGGCGTGC GGTGGGTACG GGCAGGCTAG

AGTGCGGTAG GGGAGACTGG AATTCCTGGT GTAGCGGTGA AATGCGCAGA TATCAGGAGG AACACCGATG GCGAAGGCAG GTCTCTGGGC CGTTACTGAC

ACTGAGAAGC GAAAGCATGG GGAGCGAACA GGATTAGATA CCCTGGTAGT CCATGCCGTA AACGTTGGGC ACTAGGTGTG GGGAGCATTC CACGTTTTCC

GCGCCGTAGC TAACGCATTA AGTGCCCCGC CTGGGGAGTA CGGCCGCAAG GCTAAAACTC AAAGGAATTG ACGGGGGCCC GCACAAGCGG CGGAGCATGC

GGATTAATTC GATGCAACGC GAAGAACCTT ACCAAGGCTT GACATGCACT GGATCGCTGC AGAGATGTGG TTTTCTTTGG ACTGGTGCAC AGGTGGTGCA

TGGTTGTCGT CAGCTCGTGT CGTGAGATGT TGGGTTAAGT CCCGCAACGA GCGCAACCCT CGTTCCATGT TGCCAGCACT TCGGGTGGGG ACTCATGGGA

GACTGCCGGG GTCAACTCGG AGGAAGGTGG GGACGACGTC AAATCATCAT GCCCCTTATG TCTTGGGCTT CACGCGTGCT ACAATGGTCG GTACAATGGG

TTGCGATACT GTGAGGTGGA GCTAATCCCA AAAAGCCGGT CTCAGTTCGG ATTGGGGTCT GCAACTCGAC CCTATGAAGT CGGAGTCGCT AGTAATCGCA

GATCAGCAAT GCTGCGGTGA ATACGTTCCC GGGCCTTGTA CACACCGCCC GTCAAGTCAC GAAAGTCGGT AACACCCGAA GCCGATGGCC CAAGCTTTAT

GCNGGGAGTC GTCGAAGGTG GGATCGGTGA NTGGGACTAA GTCGTAACAA GGTAGCCGTA CCGGAAGG
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FIG. 1. Nucleotide sequence of the 16S rRNA gene of strain 8 (CDC coryneform group 5).

TABLE 6. Characteristics differentiating CDC group 3 and 5 coryneform bacteria from other fermentative, nonmotile, mycolic acid-less, catalase-positive gram-positive rods[a]

Organism	Nitrate reduction	Urea hydrolysis	Esculin hydrolysis	Fermentation of[b]:					*m*-DAP[c]	Predominant CFAs
				Glu	Mal	Suc	Man	Xyl		
CDC coryneform group 3	−	−	+	+	+	+	−	+	+	$C_{ai15:0}$, $C_{ai17:0}$
CDC coryneform group 5	−	−	+	+	+	+	−	−	+	$C_{ai15:0}$, $C_{ai17:0}$
Dermabacter hominis	−	−	+	+	+	ND[d]	−	V[e]	+	$C_{ai15:0}$, $C_{ai17:0}$
Brachybacterium faecium	V	V	+	+	+	V	ND	ND	+	$C_{ai15:0}$, $C_{ai17:0}$
Actinomyces viscosus	+	V	V	+	+	+	−	V	−	$C_{16:0}$, $C_{18:0}$
Rothia dentocariosa	+	−	+	+	+	+	−	−	−	$C_{ai15:0}$, $C_{ai17:0}$
Propionibacterium avidum/granulosum	−	−	V	+	V	+	−	−	+	$C_{i15:0}$, $C_{ai15:0}$

[a] Data compiled from references 3, 7, 16, 17, 19, 22, and 31.
[b] Glu, glucose; Mal, maltose; Suc, sucrose; Man, mannitol; Xyl, xylose.
[c] *m*-DAP, *meso*-diaminopimelic acid.
[d] ND, no data.
[e] V, variable.

approximately 600 nucleotides, both group 3 and group 5 strains exhibited 99% 16S rRNA sequence similarity with *D. hominis*, indicating that these taxa are genealogically very closely related. Quantitative DNA-DNA hybridization studies may reveal whether group 3 and group 5 are identical to *D. hominis* or represent closely related species or subspecies (32). Jones and Collins (19) had already described the xylose fermentation of *D. hominis* as variable, and it is therefore unlikely that group 3 and group 5 represent different species. Finally, further case reports are needed to establish the pathogenic potential of *Dermabacter* isolates.

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